Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Original) A family A DNA polymerase which has a modified motif C sequence and an enhanced mismatch discrimination as compared to the corresponding wild type polymerase, or a Klenow fragment thereof, wherein in the motif C sequence QVH in positions 879-881, based on the *E. coli* DNA polymerase Klenow fragment shown in SEQ ID NO: 2, at least the amino acid residue Q879 has been replaced by a lipophilic amino acid residue.

2. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 1, wherein the DNA polymerase is a bacterial DNA polymerase.

3.-5. (Canceled)

6. (Withdrawn) A DNA sequence which encodes for a DNA polymerase or its Klenow fragment according to claim 1.

7. (Withdrawn) A vector comprising the DNA sequence according to claim 6.

8. (Withdrawn) A host cell which has been transformed with the vector according to claim 7.

9. (Withdrawn) A method for the preparation of a DNA polymerase or its Klenow fragment, comprising culturing a host cell according to claim 8 and isolating the DNA polymerase or the Klenow fragment from the culture or the culture supernatant.

10.-13. (Canceled)

14. (Previously Presented) A kit for determining the presence or absence of at least one sequence variant in one or more target nucleic acids in an individual sample, comprising at least one DNA polymerase according to claim 1.

15. (Previously Presented) The kit according to claim 14, additionally containing one or more of the following components:

- one or more discriminating primers containing at least one discriminating nucleotide residue, wherein the sequence variant to be detected in the target nucleic acid is complementary to at least one 3'-terminal, 3'-proxi-terminal or 3'-proxi-proxi-terminal nucleotide residue of the discriminating primer;
- one or more other primers which are complementary to a primer extension product formed by extension of said discriminating primers;
- deoxynucleoside triphosphates;
- buffers;
- quantification reagents; and
- polymerase-blocking antibodies.

16. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 2, wherein the DNA polymerase is a thermostable DNA polymerase.

17. (Currently Amended) The DNA polymerase or its Klenow fragment according to claim 16, wherein the DNA polymerase is a polymerase selected from the group consisting of polymerases from *E. coli, Aquifex, Borrelia, Bacillus, Chlamydia, Chlamydophila, Chloroflexus, Haemophilus, Heliobacter, Lactococcus, Methylobacterium, Mycobacterium, Rhodothermus, Rickettsia, Streptococcus, Streptomyces, Synechocystis, Treponema, Thermus aquaticus, Thermus thermophilus, Thermus filiformis, Rhodothermus obamensis* and *Bacillus stearothermophilus*.

18. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 1, wherein said lipophilic amino acid residue is selected from the group of residues consisting of Gly, Ala, Val, Leu, Ile, Pro, Phe, Met and Trp.

19. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 18, wherein said lipophilic amino acid residue is selected from the group of residues consisting of Gly, Ala, Val, Leu, and Ile.

20. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 1, wherein in the motif C sequence QVH in positions 879-881, H881 has been further replaced by a lipophilic amino acid residue.

21. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 20, wherein said lipophilic amino acid residue is selected from the group of residues consisting of Gly, Ala, Val, Leu, Ile, Pro, Phe, Met and Trp.

22. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 21, wherein said lipophilic amino acid residue is selected from the group of residues consisting of Gly, Ala, Val, Leu and Ile.

23. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 1, wherein in the motif C sequence QVH in positions 879-881, the amino acid residue in position 880 is selected from the group of residues consisting of Val, Leu, Ile, Ala and Tyr.

24. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 23, wherein the amino acid residue in position 880 is selected from the group of residues consisting of Val and Ile.

25. (Previously Presented) The DNA polymerase or its Klenow fragment according to claim 1, wherein the motif C sequence QVH has been replaced by a sequence selected from the group consisting of LVL and LVG.

26. (Previously Presented) The DNA polymerase according to claim 1, wherein the DNA polymerase is a Taq polymerase with the sequence shown in SEQ ID NO: 4 in which the sequence QVH in positions 782-784 has been replaced by a sequence selected from the group consisting of LVL and LVG.

27. (Previously Presented) The Klenow fragment according to claim 1, wherein the Klenow fragment comprises the sequence shown in SEQ ID NO: 2 in which the sequence QVH in positions 879-881 has been replaced by a sequence selected from the group consisting of LVL and LVG.

28. (Withdrawn) A method for performing a nucleic acid extension reaction, comprising extending a DNA primer in the presence of the DNA polymerase or its Klenow fragment of claim 1.

29. (Withdrawn) The method of claim 28 wherein the nucleic acid extension reaction is selected from the group consisting of allele-specific PCR, DNA amplification by means of PCR, and cloning.

30. (Withdrawn) The method of claim 28, wherein the method is suitable for determining the presence or absence of at least one sequence variant in one or more target nucleic acids in an individual sample.

31. (Withdrawn) The method according to claim 30 including the following steps:

a) adding:

- deoxynucleoside triphosphates;

- a DNA polymerase according to claim 1;
- at least one discriminating primer containing at least one discriminating nucleotide residue, wherein a primer is added for each sequence variant to be detected of a target nucleic acid, which primer has a sequence complementary to the sequence variant to be detected, and wherein the sequence variant to be detected in the target nucleic acid is complementary to at least one 3'-terminal, 3'-proxi-terminal or 3'-proxi-proxi-terminal nucleotide residue of the discriminating primer;
- at least one other primer which is complementary to a primer extension product formed by extension of the discriminating primer;

b) performing a primer extension reaction wherein an extension product of the discriminating primer is obtained substantially only if the sample contains a target nucleic acid with the sequence variant to be detected;

c) separating the extension product of the primer extension reaction from its template nucleic acid;

d) reiterating steps b) and c) to obtain an amplification product; and

e) determining the presence or absence of a sequence variant from the presence or absence of the amplification product.

32. (Withdrawn) The method according to claim 31, wherein steps b) to e) are performed as real-time PCR or real-time RT-PCR.

33. (Previously Presented) The kit of claim 15, wherein the quantification reagents are selected from the group consisting of intercalating reagents and reagents binding to the minor groove of a double-stranded DNA molecule.

34. (Previously Presented) The kit of claim 15, wherein the polymerase-blocking antibody is TaqBlock.